OIPE JG161
OCT 1 3 2004
PATENT & TRADEMARK OFFICE

ID two or more biological molecules

Encode molecules into character strings

Select substrings

ID two or more biological molecules

Apply Selection Criteria ? — Yes → Select concatenated strings metting slection criteria

No

Introduce variation? — Yes → Create variation string? — Yes → Create variation string

No

Run variation operator? — Yes → Run variation operator

No

No

Add string(s) to data structure? — Yes → Add string to data structure

No

Yes ← Iterate again?

No

FIG. 1

Initial strings A, B, and C:

String A:	A1 - A2 - A3 - A4 - A5
String B:	B1 - B2 - B3 - B4 - B5
String C:	C1 - C2 - C3 - C4 - C5

Select substrings

String Pools:

Pool 1:	A1, B1, C1
Pool 2:	A2, B2, C2
Pool 3:	A3, B3, C3

Concatenate substrings

New Strings:

String A:	A1 - A2 - A3 - A4 - A5
String B:	B1 - B2 - B3 - B4 - B5
String C:	C1 - C2 - C3 - C4 - C5

FIG. 2

Initial sequences
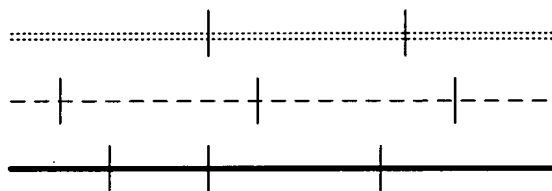
Subsequences aligned
by similarity
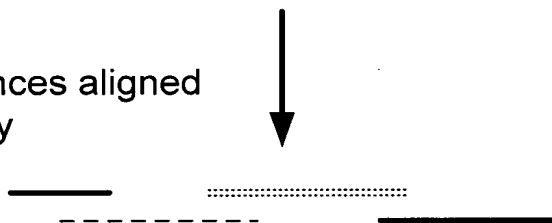
Concatenated
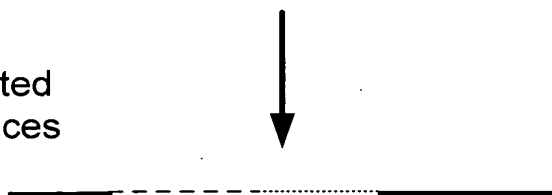subsequences

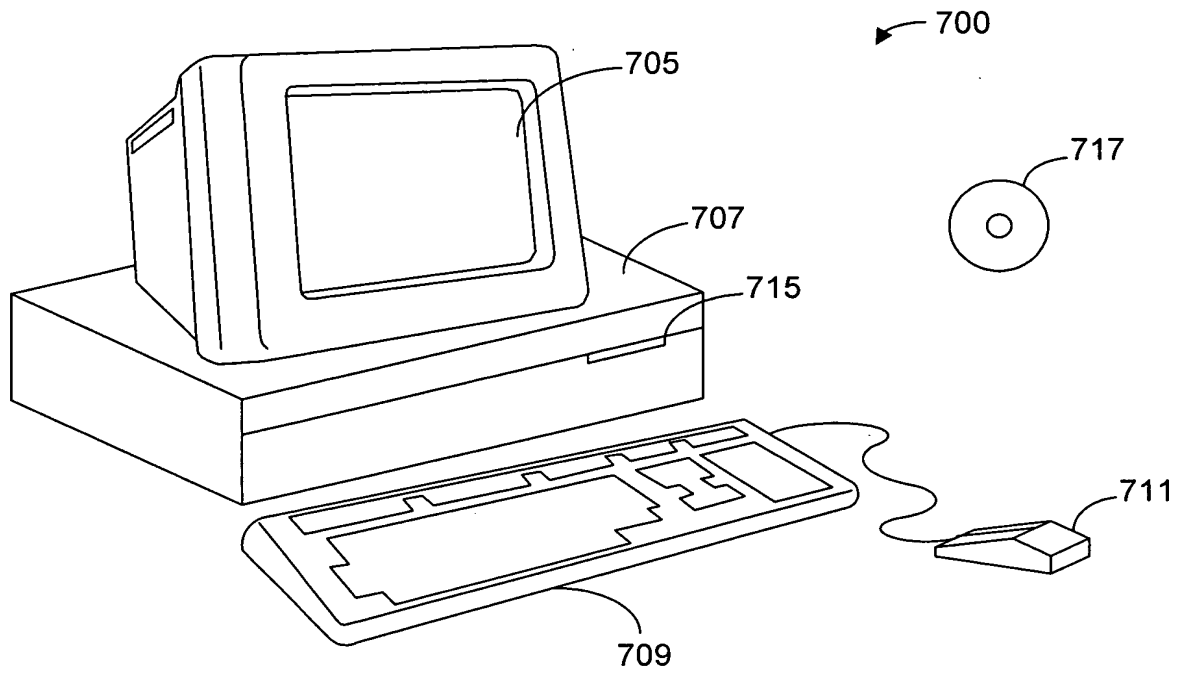**FIG. 3**

700

705

707

715

717

711

709

FIG. 4

FAMILY GAGGS MODEL # 1.

SUBTILISIN BACKGROUND INFORMATION:

7 PARENTS, SERINE PROTEASES, DIVERSE

TYPE OF ALIGHMENT/SIMILARITY DATA PRESENTED:
AMINOACID SEQUENCES, LEADER PEPTIDE EXCLUDED.

Percent Similarity

	1	2	3	4	5	6	7		
1		62.1	81.4	57.6	81.8	56.1	59.1	1	A27211 synthetic 309.PM
2	50.5		61.0	54.9	59.5	58.2	60.8	2	BACAPRQ subtilisin.PM
3	21.0	52.0		54.6	78.4	50.6	53.2	3	BACAPRS subtilisin.PM
4	54.4	63.3	62.3		52.0	64.6	67.9	4	BACSBTL subtilisin.PM
5	20.5	54.9	25.1	65.6		53.9	56.5	5	BACYAB subtilisin alk.PM
6	58.6	56.6	72.2	44.2	63.4		94.9	6	BLSC11594 subtilisin.PM
7	52.5	51.4	66.0	38.5	57.8	4.9		7	I82494 keratinase.PM
	1	2	3	4	5	6	7		

BACAPRS subtilisin.PM
BACYAB subtilisin alk.PM
A27211 synthetic 309.PM
BLSC11594 subtilisin.PM
I82494 keratinase.PM
BACSBTL subtilisin.PM
BACAPRQ subtilisin.PM

45.8

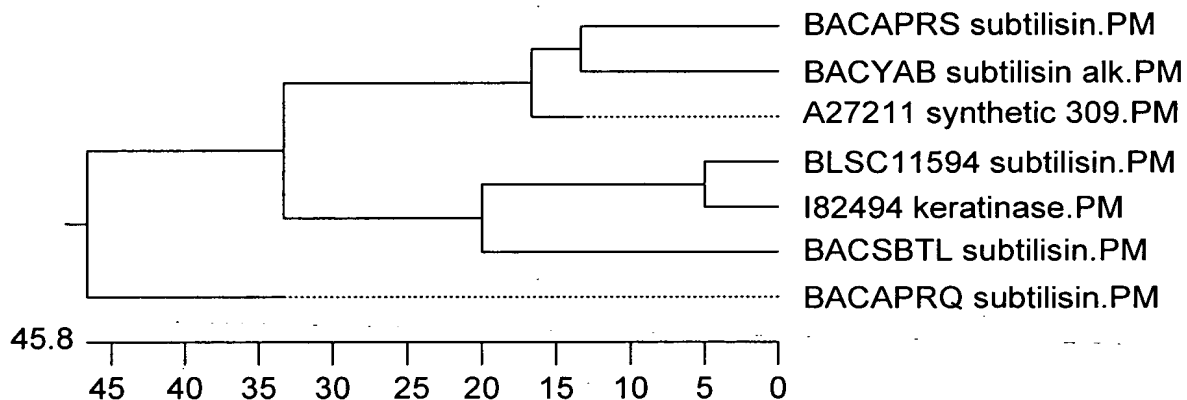45   40   35   30   25   20   15   10   5   0

FIG. 5

FAMILY GAGGS: SUBTILISIN MODEL. PAIRWISE DOT-PLOT ALIGNMENTS TO FIND HOMOLOGY AREAS
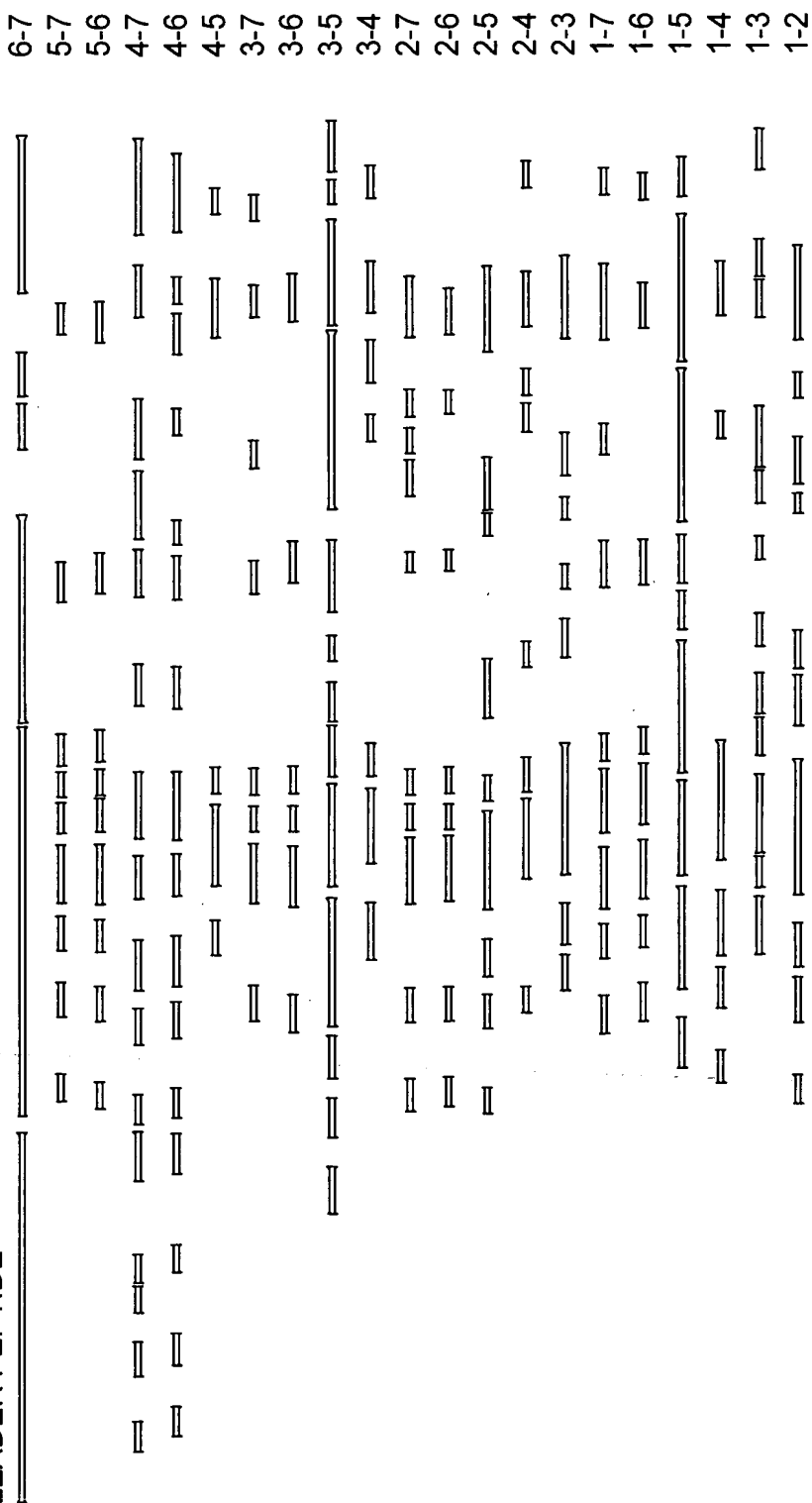
LEADER PEPTIDE

FIG. 6

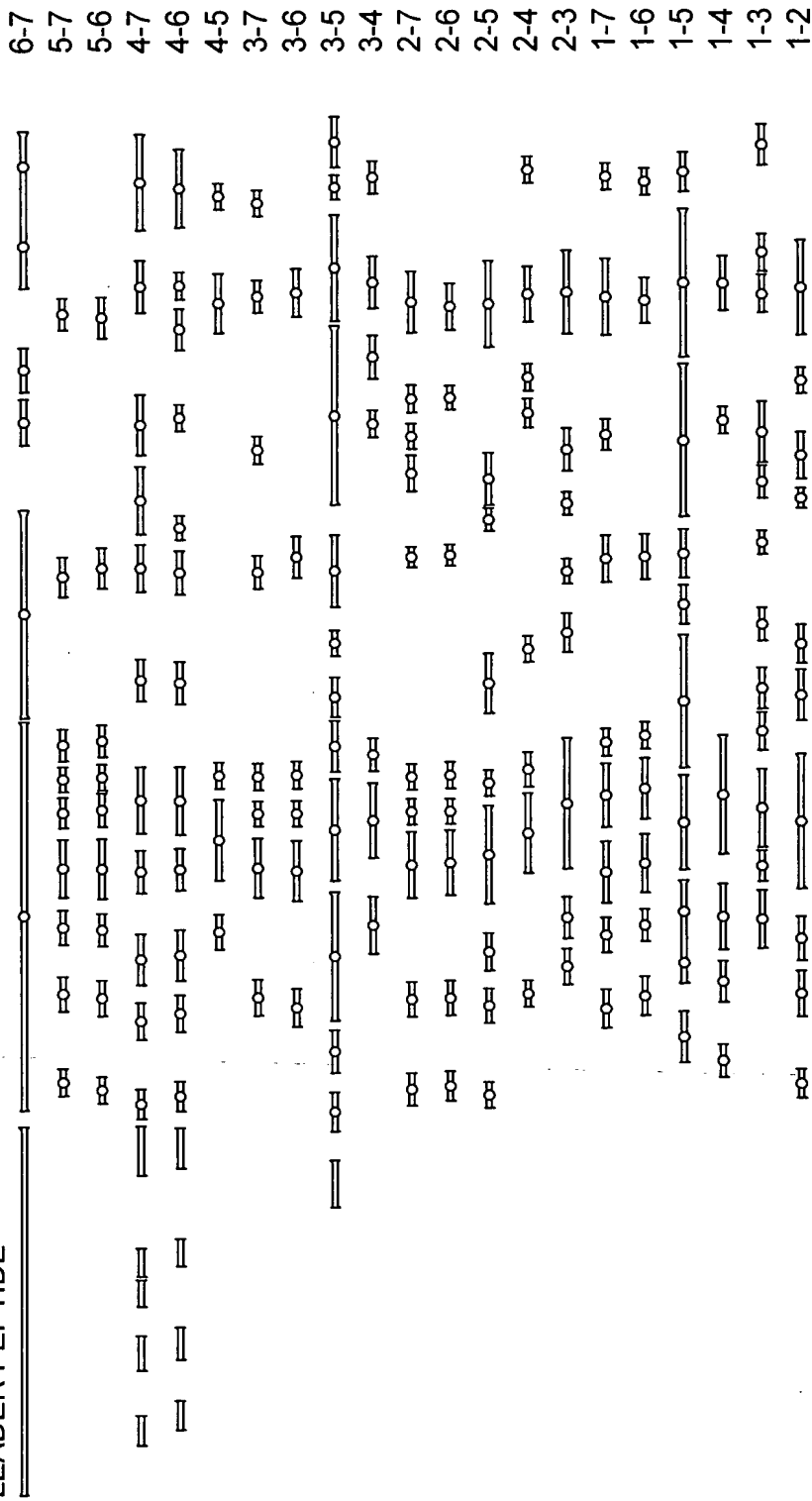GAGGS - SUBTILISIN MODEL (7 PARENTS) SELECTING PAIRWISE CROSSOVER POINTS

LEADER PEPTIDE

FIG. 7